SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Rhode, Peter R.
                Acevdo, Jorge
                Burkhardt, Martin
                Jiao, Jin-an
                Wong, Hing C.

(ii) TITLE OF THE INVENTION: SOLUBLE MHC COMPLEXES AND
        METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:
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    (B) STREET: 130 Water Street
    (C) CITY: Boston
    (D) STATE: MA
    (E) COUNTRY: USA
    (F) ZIP: 02109

(v) COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Diskette
    (B) COMPUTER: IBM Compatible
    (C) OPERATING SYSTEM: DOS
    (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE:
    (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:
    (A) NAME: Corless, Peter F
    (B) REGISTRATION NUMBER: 33,860
    (C) REFERENCE/DOCKET NUMBER: 46561

(ix) TELECOMMUNICATION INFORMATION:
    (A) TELEPHONE: 617-523-3400
    (B) TELEFAX: 617-523-6440
    (C) TELEX:

    (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 8 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCACCATG   8

          (2) INFORMATION FOR SEQ ID NO:2:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 43 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCCCAAGC TTCCGGGCCA CCATGGCTCT GCAGATCCCC AGC   43

          (2) INFORMATION FOR SEQ ID NO:3:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 34 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCCCACTT AAGGTCCTTG GGCTGCTCAG CACC   34

          (2) INFORMATION FOR SEQ ID NO:4:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 37 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGGGGCCA TGGCCGGAAA CTCCGAAAGG CATTTCG   37

          (2) INFORMATION FOR SEQ ID NO:5:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 32 base pairs
          (B) TYPE: nucleic acid

        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCGACTA GTCCACTCCA CAGTGATGGG GC   32

        (2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGGGGGCCA TGGCCGAAGA CGACATTGAG GCCGAC   36

        (2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 32 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGACTAG TCCAGTGTTT CAGAACCGGC TC   32

        (2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGGGGGATA TCTCTCAGGC TGTTCACGCT G   31

        (2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 46 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGGGTTCG AAAAGTGTAC TTACGGGGGG CTGGAATCTC AGGTTC   46

    (2) INFORMATION FOR SEQ ID NO:10:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 37 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGGGGCTCG AGTATCAAAG AAGAACATGT GATCATC   37

    (2) INFORMATION FOR SEQ ID NO:11:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 36 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGGCGGGAT CCGTTCTCTG TAGTCTCTGG GAGAGG   36

    (2) INFORMATION FOR SEQ ID NO:12:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 42 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATAAGAGGA AGAAGAGTAC ATGCCGATGG AACCCGGGTG AG   42

    (2) INFORMATION FOR SEQ ID NO:13:

  (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 43 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATTCTTCAC CCGGGTTCCA TCGGCATGTA CTCTTCTTCC TCG   43

    (2) INFORMATION FOR SEQ ID NO:14:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 75 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCCCCGCTA GCGGAGGGGG CGGAAGCGGC GGAGGGGGGG ACACCCGACC ACGTTTCCTG   60
TGGCAGCCTA AGAGG   75

    (2) INFORMATION FOR SEQ ID NO:15:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 48 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCCCCCGAAT TCCCCACTAG TCCATTCCAC TGTGAGAGGG CTTGTCAC   48

    (2) INFORMATION FOR SEQ ID NO:16:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 35 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGGGGGGCCA TGGCCTACGA CAGAACCCCG TGGTG   35

    (2) INFORMATION FOR SEQ ID NO:17:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 32 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGGGACTA GTTCGCCGCT GCACTGTGAA GC   32

          (2) INFORMATION FOR SEQ ID NO:18:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGGGGTATG CATACGACGA GAACCCCGTG GTG   33

          (2) INFORMATION FOR SEQ ID NO:19:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGGGGACTA GTCCACTTCG AGGAACTGTT TCC   33

          (2) INFORMATION FOR SEQ ID NO:20:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCCTGGTC TCCTCTGTGA GTGG   24

          (2) INFORMATION FOR SEQ ID NO:21:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCACTCACAG AGGAGACCAG GAGG   24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 30 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCCCCACCG GTTACGACAA GCCCGTGGTG   30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 45 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCCCCCATCG ATAAGTGTAC TTACGTGGGA GAGGGCTTGG AGCAT   45

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 1508 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(ix) FEATURE:

   (A) NAME/KEY: Coding Sequence
   (B) LOCATION: 6...1505
   (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCACC ATG GCT CTG CAG ATC CCC AGC CTC CTC CTC TCA GCT GCT GTG GTG   50
      Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val
      1   5   10   15

GTG CTG ATG GTG CTG AGC AGC CCA AGG ACC TTA AGT ATC TCT CAG GCT   98
Val Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln Ala
             20   25   30

GTT CAC GCT GCT CAC GCT GAA ATC AAC GAA GCT GGT CGT GCT AGC GGA   146
Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser Gly
         35   40   45

```
GGG GGC GGA AGC GGC GGA GGG GGA AAC TCC GAA AGG CAT TTC GTG GTC        194
Gly Gly Gly Ser Gly Gly Gly Gly Asn Ser Glu Arg His Phe Val Val
        50                      55                  60

CAG TTC AAG GGC GAG TGC TAC TAC ACC AAC GGG ACG CAG CGC ATA CGG        242
Gln Phe Lys Gly Glu Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile Arg
        65                      70                  75

CTC GTG ACC AGA TAC ATC TAC AAC CGG GAG GAG TAC GTG CGC TAC GAC        290
Leu Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr Asp
80                      85                  90                  95

AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CCA GAC        338
Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro Asp
                100                 105                 110

GCC GAG TAC TGG AAC AGC CAG CCG GAG ATC CTG GAG CGA ACG CGG GCC        386
Ala Glu Tyr Trp Asn Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg Ala
                115                 120                 125

GAG GTG GAC ACG GCG TGC AGA CAC AAC TAC GAG GGG CCG GAG ACC AGC        434
Glu Val Asp Thr Ala Cys Arg His Asn Tyr Glu Gly Pro Glu Thr Ser
            130                 135                 140

ACC TCC CTG CGG CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC        482
Thr Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser
        145                 150                 155

AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA        530
Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr
160                 165                 170                 175

GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG        578
Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln
                180                 185                 190

GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC        626
Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp
                195                 200                 205

TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA        674
Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly
            210                 215                 220

GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC        722
Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile
        225                 230                 235

ACT GTG GAG TGG ACT AGT GGT GGC GGT GGC AGC GGC GGT GGT GGT TCC        770
Thr Val Glu Trp Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
240                 245                 250                 255

GGT GGC GGC GGT TCT GGC GGT GGC GGT TCC TCG AGT GAA GAC GAC ATT        818
```

```
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Glu Asp Asp Ile
            260                 265             270

GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT TAT CAG TCT CCT      866
Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
            275                 280             285

GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TTG TTC      914
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
            290                 295             300

TAT GTG GAC TTG.GAT AAG AAG AAA ACT GTC TGG AGG CTT CCT GAG TTT      962
Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
            305                 310             315

GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG CAA AAC ATA GCT     1010
Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
320                 325                 330             335

GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG TCA AAT TTC ACC     1058
Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr
            340                 345             350

CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT     1106
Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
      .     355                 360             365

GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC     1154
Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile
            370                 375             380

TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC     1202
Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
            385                 390             395

ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC CGT GAC CAT TCC     1250
Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
400                 405                 410                 415

TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAT GAT GAC ATT     1298
Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
            420                 425             430

TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA     1346
Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
            435                 440             445

CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAA ACT     1394
His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
            450                 455             460

GTG GTG TGT GCC CTG GGG TTG TCT GTG GGC CTT GTG GGC ATC GTG GTG     1442
Val Val Cys Ala Leu Gly Leu Ser Val Gly Leu Val Gly Ile Val Val
            465                 470             475
```

```
GGC ACC ATC TTC ATC ATT CAA GGC CTG CGA TCA GGT GGC ACC TCC AGA      1490
Gly Thr Ile Phe Ile Ile Gln Gly Leu Arg Ser Gly Gly Thr Ser Arg
480                     485                 490                 495


CAC CCA GGG CCT TTA TGA                                               1508
His Pro Gly Pro Leu
                500
```

(2) INFORMATION FOR SEQ ID NO:25:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 500 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein
   (v) FRAGMENT TYPE: internal

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Met Ala Leu Gln Ile Pro Ser Leu Leu Leu Ser Ala Ala Val Val Val
1               5               10              15
Leu Met Val Leu Ser Ser Pro Arg Thr Leu Ser Ile Ser Gln Ala Val
        20              25              30
His Ala Ala His Ala Glu Ile Asn Glu Ala Gly Arg Ala Ser Gly Gly
        35              40              45
Gly Gly Ser Gly Gly Gly Gly Asn Ser Glu Arg His Phe Val Val Gln
    50              55              60
Phe Lys Gly Glu Cys Tyr Tyr Thr Asn Gly Thr Gln Arg Ile Arg Leu
65              70              75              80
Val Thr Arg Tyr Ile Tyr Asn Arg Glu Glu Tyr Val Arg Tyr Asp Ser
            85              90              95
Asp Val Gly Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg Pro Asp Ala
            100             105             110
Glu Tyr Trp Asn Ser Gln Pro Glu Ile Leu Glu Arg Thr Arg Ala Glu
            115             120             125
Val Asp Thr Ala Cys Arg His Asn Tyr Glu Gly Pro Glu Thr Ser Thr
    130             135             140
Ser Leu Arg Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg
145             150             155             160
Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp
            165             170             175
Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu
            180             185             190
Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp
            195             200             205
Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu
    210             215             220
Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr
225             230             235             240
Val Glu Trp Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
```

```
                 245                    250                    255
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser Glu Asp Asp Ile Glu
        260                    265                    270
Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly
        275                    280                    285
Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr
    290                    295                    300
Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly
305                    310                    315                    320
Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala
                325                    330                    335
Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro
            340                    345                    350
Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val
        355                    360                    365
Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe
    370                    375                    380
Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr
385                    390                    395                    400
Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe
                405                    410                    415
His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr
            420                    425                    430
Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His
        435                    440                    445
Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val
    450                    455                    460
Val Cys Ala Leu Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly
465                    470                    475                    480
Thr Ile Phe Ile Ile Gln Gly Leu Arg Ser Gly Gly Thr Ser Arg His
                485                    490                    495
Pro Gly Pro Leu
        500
```

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 16 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 15 amino acids
      (B) TYPE: amino acid

```
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (ii)  MOLECULE TYPE: protein

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Pro Tyr Ser Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro
 1               5                  10                  15


        (2)  INFORMATION FOR SEQ ID NO:28:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 20 amino acids
        (B)  TYPE: amino acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (ii)  MOLECULE TYPE: protein

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:28:

Tyr Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro
 1               5                  10                  15
Arg Thr Pro Pro
            20


        (2)  INFORMATION FOR SEQ ID NO:29:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 14 amino acids
        (B)  TYPE: amino acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (ii)  MOLECULE TYPE: protein

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Ser
 1               5                  10


        (2)  INFORMATION FOR SEQ ID NO:30:

    (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 11 amino acids
        (B)  TYPE: amino acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (ii)  MOLECULE TYPE: protein

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:30:
```

```
Glu Glu Glu Glu Tyr Met Pro Met Glu Pro Gly
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 24 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
TSGGGGSGGG GSGGGGSGGG GSSS                                          24
```

(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 19 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg
1               5               10              15
Thr Pro Pro
```

(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 45 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro Ser Ala
1               5               10              15
Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu
            20                  25                  30
Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
        35                  40                  45
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 44 amino acids
   (B) TYPE: amino acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Ser Ser Ala Asp Leu Val Pro Arg Gly Ser Thr Thr Ala Pro Arg Ala
 1               5                  10                 15
Gln Leu Lys Lys Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu
            20                  25                 30
Lys Trp Lys Leu Gln Ala Leu Lys Lys Leu Ala Gln
        35                  40
```

    (2) INFORMATION FOR SEQ ID NO:35:

   (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 10 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ASSGGGSGGG   10